



X12279.ST25.txt
SEQUENCE LISTING

<110> Huang, Lihua

Riggin, Ralph M

<120> HUMAN PROTEIN C POLYPEPTIDE

<130> X-12279

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1245

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: recombinant human protein c truncated at C-terminus

<220>

<221> CDS

<222> (1)..(1245)

<223>

<400> 1

gcc aac tcc ttc ctg gag gag ctc cgt cac agc agc ctg gag cg⁴⁸
Ala Asn Ser Phe Leu Glu Glu Leu Arg His Ser Ser Leu Glu Arg Glu
1 5 10 15

tgc ata gag gag atc tgt gac ttc gag gag gcc aag gaa att ttc caa
Cys Ile Glu Glu Ile Cys Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln 96
20 25 30

aat gtg gat gac aca ctg gcc ttc tgg tcc aag cac gtc gac ggt gac
Asn Val Asp Asp Thr Leu Ala Phe Trp Ser Lys His Val Asp Gly Asp 144
35 40 45

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cag tgc ttg gtc ttg ccc ttg gag cac ccg tgc gcc agc ctg tgc tgc Gln Cys Leu Val Leu Pro Leu Glu His Pro Cys Ala Ser Leu Cys Cys 50 55 60	192
ggg cac ggc acg tgc atc gac ggc atc ggc agc ttc agc tgc gac tgc Gly His Gly Thr Cys Ile Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys 65 70 75 80	240
cgc agc ggc tgg gag ggc cgc ttc tgc cag cgc gag gtg agc ttc ctc Arg Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg Glu Val Ser Phe Leu 85 90 95	288
aat tgc tcg ctg gac aac ggc ggc tgc acg cat tac tgc cta gag gag Asn Cys Ser Leu Asp Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu 100 105 110	336
gtg ggc tgg cgg cgc tgt agc tgt gcg cct ggc tac aag ctg ggg gac Val Gly Trp Arg Arg Cys Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp 115 120 125	384
gac ctc ctg cag tgt cac ccc gca gtg aag ttc cct tgt ggg agg ccc Asp Leu Leu Gln Cys His Pro Ala Val Lys Phe Pro Cys Gly Arg Pro 130 135 140	432
tgg aag cgg atg gag aag aag cgc agt cac ctg aaa cga gac aca gaa Trp Lys Arg Met Glu Lys Lys Arg Ser His Leu Lys Arg Asp Thr Glu 145 150 155 160	480
gac caa gaa gac caa gta gat ccg ccg ctc att gat ggg aag atg acc Asp Gln Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys Met Thr 165 170 175	528
agg cgg gga gac agc ccc tgg cag gtg gtc ctg ctg gac tca aag aag Arg Arg Gly Asp Ser Pro Trp Gln Val Val Leu Leu Asp Ser Lys Lys 180 185 190	576
aag ctg gcc tgc ggg gca gtg ctc atc cac ccc tcc tgg gtg ctg aca Lys Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr 195 200 205	624
gcg gcc cac tgc atg gat gag tcc aag aag ctc ctt gtc agg ctt gga Ala Ala His Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu Gly 210 215 220	672
gag tat gac ctg cgg cgc tgg gag aag tgg gag ctg gac ctg gac atc Glu Tyr Asp Leu Arg Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile 225 230 235 240	720
aag gag gtc ttc gtc cac ccc aac tac agc aag agc acc acc gac aat Lys Glu Val Phe Val His Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn 245 250 255	768
gac atc gca ctg ctg cac ctg gcc cag ccc gcc acc ctc tcg cag acc Asp Ile Ala Leu Leu His Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr 260 265 270	816
ata gtg ccc atc tgc ctc ccg gac agc ggc ctt gca gag cgc gag ctc Ile Val Pro Ile Cys Leu Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu 275 280 285	864
aat cag gcc ggc cag gag acc ctc gtg acg ggc tgg ggc tac cac agc Asn Gln Ala Gly Gln Glu Thr Leu Val Thr Gly Trp Gly Tyr His Ser 290 295 300	912

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agc cga gag aag gag gcc aag aga aac cgc acc ttc gtc ctc aac ttc Ser Arg Glu Lys Glu Ala Lys Arg Asn Arg Thr Phe Val Leu Asn Phe	960
305 310 315 320	
atc aag att ccc gtg gtc ccg cac aat gag tgc agc gag gtc atg agc Ile Lys Ile Pro Val Val Pro His Asn Glu Cys Ser Glu Val Met Ser	1008
325 330 335	
aac atg gtg tct gag aac atg ctg tgt gcg ggc atc ctc ggg gac cgg Asn Met Val Ser Glu Asn Met Leu Cys Ala Gly Ile Leu Gly Asp Arg	1056
340 345 350	
cag gat gcc tgc gag ggc gac agt ggg ggg ccc atg gtc gcc tcc ttc Gln Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Met Val Ala Ser Phe	1104
355 360 365	
cac ggc acc tgg ttc ctg gtg ggc ctg gtg agc tgg ggt gag ggc tgt His Gly Thr Trp Phe Leu Val Gly Leu Val Ser Trp Gly Glu Gly Cys	1152
370 375 380	
ggg ctc ctt cac aac tac ggc gtt tac acc aaa gtc agc cgc tac ctc Gly Leu Leu His Asn Tyr Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu	1200
385 390 395 400	
gac tgg atc cat ggg cac atc aga gac aag gaa gcc ccc cag aag Asp Trp Ile His Gly His Ile Arg Asp Lys Glu Ala Pro Gln Lys	1245
405 410 415	

<210> 2

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: recombinant human protein c truncated at C-terminus

<400> 2

Ala Asn Ser Phe Leu Glu Glu Leu Arg His Ser Ser Leu Glu Arg Glu	
1 5 10 15	

Cys Ile Glu Glu Ile Cys Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln	
20 25 30	

Asn Val Asp Asp Thr Leu Ala Phe Trp Ser Lys His Val Asp Gly Asp	
35 40 45	

Gln Cys Leu Val Leu Pro Leu Glu His Pro Cys Ala Ser Leu Cys Cys	
50 55 60	

Gly His Gly Thr Cys Ile Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys	
65 70 75 80	

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Arg Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg Glu Val Ser Phe Leu
85 90 95

Asn Cys Ser Leu Asp Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu
100 105 110

Val Gly Trp Arg Arg Cys Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp
115 120 125

Asp Leu Leu Gln Cys His Pro Ala Val Lys Phe Pro Cys Gly Arg Pro
130 135 140

Trp Lys Arg Met Glu Lys Lys Arg Ser His Leu Lys Arg Asp Thr Glu
145 150 155 160

Asp Gln Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys Met Thr
165 170 175

Arg Arg Gly Asp Ser Pro Trp Gln Val Val Leu Leu Asp Ser Lys Lys
180 185 190

Lys Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr
195 200 205

Ala Ala His Cys Met Asp Glu Ser Lys Lys Leu Val Arg Leu Gly
210 215 220

Glu Tyr Asp Leu Arg Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile
225 230 235 240

Lys Glu Val Phe Val His Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn
245 250 255

Asp Ile Ala Leu Leu His Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr
260 265 270

Ile Val Pro Ile Cys Leu Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu
275 280 285

Asn Gln Ala Gly Gln Glu Thr Leu Val Thr Gly Trp Gly Tyr His Ser
290 295 300

Ser Arg Glu Lys Glu Ala Lys Arg Asn Arg Thr Phe Val Leu Asn Phe
305 310 315 320

Ile Lys Ile Pro Val Val Pro His Asn Glu Cys Ser Glu Val Met Ser
325 330 335

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Asn Met Val Ser Glu Asn Met Leu Cys Ala Gly Ile Leu Gly Asp Arg
340 345 350

Gln Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Met Val Ala Ser Phe
355 360 365

His Gly Thr Trp Phe Leu Val Gly Leu Val Ser Trp Gly Glu Gly Cys
370 375 380

Gly Leu Leu His Asn Tyr Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu
385 390 395 400

Asp Trp Ile His Gly His Ile Arg Asp Lys Glu Ala Pro Gln Lys
405 410 415